FULL TITLE

Intracellular directed evolution of proteins from combinatorial libraries based on conditional phage replication

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ABSTRACT

Directed evolution is a powerful tool to improve the characteristics of biomolecules. Here we present a protocol for the intracellular evolution of proteins with distinct differences and advantages to established techniques. These include the ability to select for a particular function from a library of protein variants inside cells, minimizing undesired co-evolution and propagation of non-functional library members, as well as allowing positive and negative selection logics using basally-active promoters. A typical evolution experiment comprises the following steps: (i) Preparation of a combinatorial M13 phagemid library expressing variants of the gene of interest and the *E. coli* host cells; (ii) Multiple rounds of an intracellular selection process towards a desired activity; (iii) The characterization of the evolved target proteins. The system has been developed for the selection of new orthogonal transcription factors[1] (TFs) but is capable of evolving any gene – or gene circuit function – that can be linked to conditional M13 phage replication. Here we demonstrate our approach by the directed evolution of TFs based on λ cI against two synthetic bidirectional promoters. The evolved TF variants enable simultaneous activation and repression against their engineered promoters and do not cross-react with the wild-type promoter, thus ensuring orthogonality. This protocol requires no special equipment, allowing synthetic biologists and general users to evolve improved biomolecules within ~7 weeks.

Keywords: Directed evolution, Gene circuit engineering, Synthetic biology, Protein engineering, M13 bacteriophage, Gene networks, Logic gates, Artificial transcription factors

EDITORIAL SUMMARY This protocol describes a phagemid-based intracellular evolution approach to generate and select for proteins with improved biological characteristics.

TWEET Improving biomolecule function using an intracellular directed evolution approach.

COVER TEASER Improving biomolecules by intracellular directed evolution.

Key references:

Brödel, A.K., Jaramillo, A. & Isalan, M. Engineering orthogonal dual transcription factors for multi-input synthetic promoters. *Nature Communications* **7**, 13858 (2016).

Schaerli, Y., Munteanu, A., Gili, M.L., Sharpe, J. & Isalan M. A unified design space of synthetic stripe-forming networks. *Nature Communication*s **5**, 4905 (2014).

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INTRODUCTION

Directed evolution has emerged as a powerful tool to improve the characteristics of biomolecules[2-4]. The approach mimics natural selection to evolve biomolecules towards a desired activity[5]. One efficient and commonly-used strategy to achieve this in a laboratory environment is to employ filamentous bacteriophages such as M13, to link a mutable genotype to a selectable phenotype. In this way, a number of M13 phage-assisted methods, such as the widely-used phage display technology[6], have been developed and applied to improve a wide variety of proteins, including antibodies[7-9], DNA-binding proteins[10,11], and enzymes[12,13]. These systems are characterized by an extracellular (*in vitro*) or intracellular (*in vivo*) mode of operation. *In vitro* systems are generally easier to engineer in terms of selection stringency adjustments[14], but possess certain limitations that can only be overcome by applying intracellular processes. For example, selection from combinatorial libraries *in vivo* ensures compatibility with the host cell machinery. This facilitates the optimization of synthetic proteins and gene circuits[15-17], which ultimately have to function in a host cell context. *In vivo* methods promote selection for *orthogonality*[18,19], – a lack of cross-reactions – by intrinsically counter-selecting against adverse effects inside the cell. To further broaden the applications of *in vivo* directed evolution, we recently developed an M13 phage-based method[1] for the intracellular selection of proteins from combinatorial libraries with distinct differences and advantages to established techniques.

Overview of the protocol

This protocol describes a general approach for the directed evolution of proteins from combinatorial libraries on phagemids (**Fig. 1**). The selection process takes place inside *E. coli* cells by linking the target protein's activity to conditional phage production, thus allowing enrichment of functional library members. This is exemplified here by the directed evolution of orthogonal dual transcription factors (TFs) based on bacteriophage λ cI variants[1], selecting against synthetic promoters. However, the method can be readily adapted for other target biomolecules (see **Applications of the method**). A typical evolution experiment consists of: 1) The preparation of a combinatorial M13 phage library (steps 1-38) and *E. coli* host cells (steps 39-47); 2) The selection process towards a desired activity (steps 48-61); and 3) The characterization of the selected target proteins (steps 62-68) (**Fig. 2**).

The system is based on *E. coli* cultures and three compatible plasmids (available from Addgene; see **MATERIALS**). Together, these conditionally produce phage (containing the evolving gene) in correlation to the activity of a library member. A selection experiment

always begins with an *E. coli* culture that contains the first two plasmids: a modified helper phage plasmid (HP) and an accessory plasmid (AP) (**Fig. 3a**). The HP provides almost all that is needed for phage propagation, except for two essential genes (gIII and gVI). Furthermore, the weak M13 packaging signal (PS) is removed from the original M13KO7 HP to obtain the final M13KO7-ΔPS-ΔgIII-ΔgVI HP. The second plasmid, AP, contains a conditional gene circuit that links an inducible input (e.g. a promoter with a novel operator) to gVI expression. The evolving gene or gene circuit is placed on the third plasmid, termed a phagemid (PM), which is packaged into an infectious phage particle only when all phage genes are expressed. The PM contains the second missing gene (gIII) and a combinatorially-randomized gene of interest (GOI) and is provided to the *E. coli* culture in the form of an infectious phage library (**Fig. 3b**). Crucially, our system moves Gene III onto the phagemid so that phage replication occurs only after initial infection, thus circumventing infection resistance[20,21], and decreasing the chances of propagating non-functional library members due to multiple infections. A GOI with the desired characteristics upregulates gene VI expression on the AP, completing the phage life cycle. For example, a randomized TF library member that activates an artificial promoter upstream of gVI will increase its own phage production (**Fig. 4a**). In this way, a protein with novel desired properties can be selected after several rounds of reinfection.

Applications of the method

The method has been used to evolve a set of dual activator-repressor switches for orthogonal logic gates, based on bacteriophage λ cI variants, and multi-input promoter architectures, and these switches have been successfully applied in downstream synthetic gene circuits[1]. In general, the method is capable of evolving any gene – or gene circuit function – on the phagemid that can be linked to pVI production. This is analogous to previous uses of phage-assisted continuous evolution (PACE)[22] (**Fig. 4**). With PACE, a wide range of medically and biotechnologically relevant biomolecules, including polymerases[22], proteases[23], genome-editing proteins[11] as well as protein-protein interactions[24] were linked to conditional M13 phage propagation. In principle, any application where directed evolution approaches have been proposed (e.g. biosensors[25] or hybrids with chemical evolution[26]) can be adapted to this method if the target protein's activity can be linked to conditional M13 phage production. Although certain applications (e.g. membrane proteins) would be harder to adapt, which is why other methods such as liposome display[27] have been developed.

Comparison with other methods

Several bacterial directed evolution methods have been developed based on phage replication[22], display technologies[6,27-29], genome engineering[30], as well as conditional cell growth[31,32]. Linking a target protein's activity to cell growth is a widely-used strategy and is particularly suitable when the evolving gene directly improves cellular fitness[33,34]. The use of bacteriophage offers a convenient way to uncouple the fitness function of a cell with target protein activity. This is achieved by linking a target gene's activity to phage replication using a conditional gene circuit. The main advantage of conditional phage production over display technologies is the compatibility of target genes or gene circuits with the host cell machinery as these have to function in a host cell context. In contrast to PACE (which uses gIII as the sole conditional gene), our phagemid-based approach facilitates the selection of large combinatorial libraries and enables positive and negative selection logics using promoters with basal gene expression. Our system also minimizes the undesired co-evolution of phage genes as only the packaged phagemid is evolving and not the helper phage itself. In comparison to PACE, the protocol is performed in batch mode and therefore requires no special equipment for reactor assembly but instead relies on a daily researcher intervention during selections. Moreover, the batch process facilitates the performance of multiple selections in parallel, enabling the scalability of each individual selection and easy handling. Continuous culture evolution systems can suffer from 'phage washout' (loss of phage) when conditional phage production rates are not compatible with the flow rates. By contrast, batch modes are not as sensitive to loss of phage. On the other hand, dozens of rounds of reinfections occur in a single day of PACE whereas our system is currently limited to one round per overnight cycle. In addition, combinatorial libraries have to be designed and cloned because, unlike PACE, our system does not include a random mutagenesis plasmid[35]. This means that structural information or a partial understanding of how a set of amino acid changes will affect the target protein's activity is required to run our system.

Limitations of the phagemid-based system

The main limitation of the system is the combinatorial size of the library which is linked to transformation efficiency (10^6-10^{10} variants)[36]. The selection process itself is not limited to a certain number of gene variants but it has to be noted that the use of larger libraries comes with the cost of prolonged experiment times. Another limitation can be the linkage of the target protein's activity to conditional M13 phage replication as this depends on the individual protein's characteristics. This is certainly more complicated for complex proteins such as membrane proteins than it is for cytosolic proteins. Furthermore, general limitations of

bacterial expression over mammalian expression (e.g. protein solubility, disulfide bonds, posttranslational modifications) need to be considered for individual target proteins. For instance, our system would need to be adapted to enable the selection of proteins that require disulfide bonds for proper folding in bacterial cells[37].

Experimental Design

Combinatorial library cloning on phagemid (PM). Choosing which positions to randomize in the protein of interest is a critical step as this affects the library size, the cloning strategy, and ultimately the overall selection results. Small libraries with only one or two randomized positions can easily be obtained by round-the-world PCR whereas bigger libraries require overlap extension PCR or end-to-end ligation[36]. Round-the-world PCR means in this context, that single base pair mutations are inserted into the target region by amplification of the whole plasmid DNA with randomized primers so that no additional step for plasmid ligation is required. For round-the-world PCR, both randomized primers must contain the mutations and bind to the same DNA sequence on opposite strands of the plasmid. Primers are generally 30-60 nucleotides long (N) and contain mutations in the middle of the randomized primers, flanked with 15-20 bases of correct sequence on both sides. These primers should ideally have a minimum GC content of 40% (%GC), end with one or more C or G bases and are purified by polyacrylamide gel electrophoresis (PAGE). The annealing region should have a melting temperature (T_m) of $\geq$78°C using the following formula: $T_m = 81.5 + 0.41(\%GC) - 675/N - \%mismatch$. In this protocol, we focus on an overlap PCR approach prior to Gibson Assembly[38] as this has been our method of choice for building λ cI_{opt} libraries with a combinatorial space of >10^6 variants (**Fig. 5a**). These libraries are based on a λ cI optimized mutant (cI_{opt}) with a strong activation region[39]. The protocol presented here is optimized for the construction of combinatorial libraries using Gibson Assembly. It is our method of choice because it bypasses the need for restriction sites inside target genes which makes it much easier to construct sequence-targeted libraries. However, the selection system itself is compatible with any other library generation method[36,40] as long as our phagemid vector backbone is used. The design of randomized oligonucleotides for overlap PCR is similar to conventional Gibson primer design[38]. Briefly, PCR primers for insert amplification require a 15-25 bp overlap with each other, as well as a 15-25 bp overlap with the amplified PM vector backbone. Randomized positions should be avoided in the annealing regions and primers should ideally have a T_m of 50-60°C using the following formula: $T_m = 4(G + C) + 2(A + T)$ (where A, C, G and T are the numbers of each base in the primer). The temperature difference of the primer pairs should be matched and lie within a 5°C range. The maximum insert size is limited by oligonucleotide synthesis (currently about 120 bp; desalted

oligonucleotides are sufficiently pure). For evolving a novel protein, the user should ideally start with a crystal structure of the target molecule (if available) and randomize positions known to affect the desired activity (e.g. change positions of the binding interface in order to alter the protein binding interaction). In other cases, biochemical information might also be sufficient to guide library construction.

Accessory plasmid (AP) design. The conditional gene circuit that links an inducible input to gVI expression has to be adapted to individual needs. This is achieved by replacing the λ P_{RM} promoter (pJPC12-ΔPS-P_{RM}-B0034-gVI) with a different promoter or inducible input depending on the desired application (**Fig. 5b**). The bidirectional promoter P_R/P_{RM} consists of three operator sites (O1-O2-O3) where λ cI binding to O1-O2 leads to P_{RM} activation[41]. Counterselection via repression is achieved by putting a specific DNA sequence at operator position O3 which is located between the -35 and -10 regions. For example, the O3 site of the P_{RM} promoter can be replaced with the consensus wild-type (WT) sequence called O_{CS}. Thus, binding of a cI_{opt} library member to O1-O2 of an engineered P_M promoter activates gene VI expression (and so promotes selection) while simultaneous binding to WT O3 represses gene VI, enabling counterselection against unwanted WT activity. Positive and negative selections against the synthetic promoters $P_{M,5G6G}$ and $P_{M,5T6T}$ are depicted as examples for this protocol (**Supplementary Fig. 1**). The engineered promoters are designated according to the positions of the base substitutions in the consensus half-site of O1 and O2.

Reporter plasmid (RP) design. This protocol describes the downstream functional characterization of evolved TFs by fluorescence analysis. It has to be noted that a suitable reporter assay needs to be adapted to the target protein's properties according to the user's needs. To achieve this, the bidirectional P_R/P_{RM} promoter on the RP plasmid (pJPC12-ΔPS-mCherry-P_R/P_{RM}-GFP) has to be replaced by the same inducible input used on the AP for selection (**Fig. 5c**). The insertion of the bidirectional promoters $P/P_{M,5G6G}$ and $P/P_{M,5T6T}$ into the RP is depicted as examples for this protocol (**Supplementary Fig. 2**). For other target proteins, it might be sufficient to use one of the two reporters to analyse activity of the selected proteins.

Control selections. Enrichment assays can be performed to test the efficiency of the selection process. Mix plasmids containing λ cI_{opt} (Addgene plasmid ID: 80852) and one of the orthogonal cI variants (e.g. $cI_{5G6G,P}$; Addgene plasmid ID: 80861) in different ratios (e.g. 10^{-3} and 10^{-6}). Then transform these into TOP10 cells with the modified helper phage M13KO7-ΔPS-ΔgeneIII-ΔgeneVI and the accessory plasmid pJPC12-ΔPS-P_{RM}-B0034-geneVI. This will allow the production of a phage stock packaged with cI_{opt} and $cI_{5G6G,P}$ (steps

23-38). Use the obtained phage population and run a batch selection using the accessory plasmid pJPC12-ΔPS-P_{RM}-B0034-geneVI (steps 41-61). Enrichment of λ cI_{opt} can be monitored by infecting TG1 cells (containing the plasmid pJPC12-ΔPS-mCherry-P_R/P_{RM}-GFP; Addgene plasmid ID: 80859) with the phage titer obtained after each round of selection. Streak out infected cells on agar plates supplemented with chloramphenicol and ampicillin and grow overnight at 37°C. The next day, analyse plates under the UV light of a gel documentation system. The ratio of green to red colonies should increase over time because the non-active TF $cI_{5G6G,P}$ results in red colonies while the enriched active cI_{opt} leads to green colonies due to GFP activation and mCherry repression. As an alternative control selection, the transcription factor $cI_{5G6G,P}$ can be replaced by a reporter (e.g. a red fluorescent protein, RFP) on the PM and the selection process can be monitored by infecting TG1 cells and counting the ratio of red to white colonies after each round of selection[1].

MATERIALS

REAGENTS

Cloning and plasmid construction

- Plasmids: M13KO7-ΔPS-ΔgeneIII-ΔgeneVI (Addgene plasmid ID: 80840), pLITMUS-rpoN-cI_{opt}-J23106-geneIII (Addgene plasmid ID: 80852), pJPC12-ΔPS-P_{RM}-B0034-geneVI (Addgene plasmid ID: 80858), optional: pJPC12-ΔPS-mCherry-P_R/P_{RM}-GFP (Addgene plasmid ID: 80859), pLITMUS-rpoN-$cI_{5G6G,P}$-J23106-geneIII (Addgene plasmid ID: 80861) (**Supplementary Fig. 3, Supplementary Table 1**). Sequences of all plasmids are listed in **Supplementary Data 1-5**.
- Oligonucleotides (Sigma). Primers used for cloning are listed in **Supplementary Table 2.**
- KOD Hot Start DNA Polymerase (Merck Millipore, cat. no. 71086). PCR reaction components are listed in the Equipment Setup**.**
- Diethyl pyrocarbonate (DEPC)-treated and sterile filtered water (Sigma, cat. no. 95284)
- Gibson Assembly Master Mix (New England BioLabs, cat. no. E2611)
- DpnI endonuclease (New England BioLabs, cat. no. R0176)
- Super Optimal broth with Catabolite repression (S.O.C.) medium (Sigma, cat. no. 15544034)
- DNA Gel Loading Dye, 6× (Thermo Scientific, cat. no. R0611)
- 1 kb Plus DNA Ladder (Thermo Scientific, cat. no. 10787026)
- SYBR Safe DNA Gel Stain (Life Technologies, cat. no. S33102)
- Tris-borate-ethylenediaminetetraacetic acid (TBE) Buffer, 10× (Sigma, cat. no. T4415)
- Agarose for gel electrophoresis (Sigma, cat. no. A9539)

- QIAquick Gel Extraction Kit (Qiagen, cat. no. 28704)
- QIAquick PCR Purification Kit (Qiagen, cat. no. 28104)
- MinElute PCR Purification Kit (Qiagen, cat. no. 28004)
- QIAprep Spin Miniprep Kit (Qiagen, cat. no. 27104)
- HiSpeed Plasmid Maxi Kit (Qiagen, cat. no. 12663)

Strains, buffers and media

- One Shot Chemically Competent TOP10 *E. coli* (Fisher Scientific, cat. no. C404010)
- Mix & Go Competent Cells - Strain TG1 (Zymo Research, cat. no. T3017)
- 5-alpha Electrocompetent *E. coli*, optional (New England BioLabs, cat. no. C2989K)
- Lysogeny broth (LB) with agar (Sigma, cat. no. L2897)
- Ampicillin (Sigma, cat. no. A0166), chloramphenicol (Sigma, cat. no. C0378), kanamycin (Sigma, cat. no. K4000), carbenicillin disodium salt (Sigma, cat. no. C1389)
- 2× tryptone yeast extract (2×TY): NaCl (Sigma, cat. no. S9888), yeast extract (Sigma, cat. no. Y1625), tryptone (Sigma, cat. no. T7293)
- Glycerol (Sigma, cat. no. G5516)
- Ethanol (≥ 99.8%) for molecular biology (Merck Millipore, cat. no. 1085430250)
- M9 Minimal Salts, 5× (Sigma, cat. no. M6030)
- M9 plates: bacteriological agar (Sigma, cat. no. A5306), $MgSO_4$ (Sigma, cat. no. M7506), D-(+)-glucose (Sigma, cat. no. G8270), $CaCl_2$ (Sigma, cat. no. C1016), thiamine-HCl (Sigma, cat. no. T1270)

EQUIPMENT

- Polymerase chain reaction (PCR) tubes (VWR, cat. no. 732-0545)
- Microcentrifuge tubes (1.5 ml; Thermo Scientific, cat. no. 05-408-129)
- Conical centrifuge tube, polypropylene, 15 ml (BD Falcon, cat. no. 352097)
- Conical centrifuge tubes, polypropylene, 50 ml (Corning, cat. no. 430829)
- Schott culture flasks, 250 ml (Sigma, cat. no. Z620033)
- Nunc CryoTubes (Thermo Scientific, cat. no. 366656)
- Serological pipettes (5 ml, 10 ml, and 25 ml; Fisher Scientific, cat. nos. 13-678-11D, 13-678-11E and 13-678-11)
- Sterile filters (0.22 µm pore size, Millex-GV, cat. no. SLGV033RS)
- L-shaped cell spreaders (Fisher Scientific, cat. no. 14-665-231)
- Cell culture centrifuge Avanti J-26XP (Beckman Coulter, cat. no. 393124)
- Microcentrifuge (Eppendorf, 5415D)

- Dri-block heater (Techne, DB100/2)
- Eppendorf Thermomixer Compact (Sigma, cat. no. T1317)
- Balance Sartorius Excellence (Sartorius)
- NanoDrop Lite Spectrophotometer (Thermo Scientific)
- Biophotometer (Eppendorf)
- Biophotometer cuvettes (Sigma, cat. no. Z605050)
- Horizontal gel electrophoresis systems (Bio-Rad)
- Gel documentation system (InGenius 3, Syngene)
- Gene Pulser Cuvette, 0.1 cm electrode (Bio-Rad, cat. no. 165-2089)
- Gene Pulser Xcell Microbial System (Bio-Rad, cat. no. 1652662)
- PCR thermocycler (Bio-Rad S1000, cat. no. 1852196)
- Petri dishes, 57 cm^2 (Sigma, cat. no. P7741)
- Mini Incubator (Labnet International, I5110A)
- Nunc Square BioAssay Dishes, 24.1 cm × 24.1 cm (Thermo Scientific, cat. no. 10570502)
- Shaking Incubator SI500 (Stuart)
- Cell culture microplate, 96 well, optional (Greiner Bio-One, cat. no. 655090)
- Infinite M200 plate reader, optional (Tecan)
- Research pipettes: 10 µl, 100 µl, 1000 µl (Sigma, cat. no. Z683884)
- Tips: 10 µl, 200 µl, 1000 µl (Starlab, cat. nos. S1111-3700-C, S1113-1700-C, S1111-6701-C)

REAGENT SETUP

Antibiotic stocks Prepare 100 mg ml^{-1} ampicillin in H_2O (sterile filtered), 100 mg ml^{-1} kanamycin in H_2O (sterile filtered) and 100 mg ml^{-1} chloramphenicol in ethanol. Aliquot stocks into sterile 1.5 ml tubes and store at -20°C for up to 6 months. The final concentrations, if not stated otherwise, are 100 µg ml^{-1} ampicillin (1:1000), 50 µg ml^{-1} kanamycin (1:2000), and 25 µg ml^{-1} chloramphenicol (1:4000).

Glycerol Prepare a sterile 10% (v/v) glycerol solution in H_2O for making electrocompetent cells. Glycerol stocks are obtained by preparing a sterile 50% (v/v) glycerol solution in H_2O and adding glycerol to the cell culture (f.c. 20% (v/v)) prior to freezing at -80°C. Store glycerol stock at 4°C for up to 3 months.

TBE electrophoresis buffer Dilute TBE buffer in distilled water to a 1× working solution and store at room temperature (15-25°C) for up to 6 months.

Culture medium Autoclave 2×TY medium (5 g l^{-1} NaCl, 10 g l^{-1} yeast extract, 16 g l^{-1} tryptone) and add antibiotics where appropriate before use. Store medium at 4°C for up to several months.

LB plates Add 35 g LB powder in 1 l water and autoclave. Add antibiotics where appropriate, pour into petri dishes and allow to solidify. Store plates at 4°C for up to several weeks. Note that antibiotics degrade over time which might affect the concentration when stored for prolonged times.

M9 minimal medium plates Autoclave 7 g bacteriological agar in 500 ml 1x M9 medium. Add 1 ml 1M $MgSO_4$ (autoclaved), 5 ml 20% (w/v) D-(+)-glucose (sterile filtered), 50 µl 1M $CaCl_2$ (autoclaved) and 500 µl 1M thiamine-HCl (sterile filtered) to M9 agar just before use. Add antibiotics where appropriate. Store plates at 4°C for up to several months.

EQUIPMENT SETUP

PCR thermocycler The PCR reaction components are listed below.

Component	Volume [µl]	Final concentration
10× Buffer	5	1×
25 mM $MgSO_4$	3	1.5 mM
dNTPs (2 mM each)	5	0.2 mM (each)
H_2O	varies	
Forward primer (5 µM)	3	0.3 µM
Reverse primer (5 µM)	3	0.3 µM
Template DNA	varies	0.02-0.2 ng/µl
KOD DNA Polymerase (1 Unit/µl)	1	0.02 U/µl
Total reaction volume	50	

CRITICAL: For targets greater than 2 kb, final Mg^{2+} concentrations are adjusted to 2mM.

The following conditions are used for all PCR reactions:

Step	Conditions
1. Polymerase activation	95°C, 2 min
2. Denature	95°C, 30 s
3. Annealing	temperature *varies*, 30 s
4. Extension	70°C, time *varies*
Repeat steps 2.-4.	Number of cycles *vary*
Final extension	70°C, 10 min
Infinite hold	4°C

See **Supplementary Table 3** for PCR conditions specific for individual reactions.

Infinite M200 plate reader Temperature: 37°C, duration: 10 h, shaking: 281 r.p.m., absorbance: 600 nm +/- 9 nm, fluorescence mCherry: excitation 585 nm +/- 9 nm; emission 625 nm +/- 20 nm; gain value 70, fluorescence GFP: excitation 485 nm +/- 9 nm; emission 520 nm +/- 20 nm; gain value 40.

PROCEDURE

Phagemid construction by Gibson Assembly • TIMING 2 weeks

1. Design and order generic forward and reverse primers (e.g. pLITMUS-F and pLITMUS-R; **Supplementary Table 2**) for the amplification of the PM vector backbone (pLITMUS-rpoN-cI_{opt}-J23106-geneIII) upstream of cI_{opt} and downstream the terminator BBa_B0015. Note that the terminator BBa_B0015 occurs twice in the parental plasmid. The "medium strength" rpoN promoter is used to express the evolving gene to achieve a balance between functional expression and any potential metabolic load. The levels of the expressed target gene may need to be adjusted to the function in other cases.
2. Design and order user-specific primers (e.g. cI-F and cI-R; **Supplementary Table 2**) for the gene of interest plus terminator of choice (e.g. BBa_B0015) with a 15-25 bp overlap to the PM vector backbone.
3. Amplify the gene of interest and vector backbone by PCR (See Equipment Setup) and purify the samples using the QIAquick PCR Purification Kit. ▲CRITICAL STEP If the PCR reactions contain unwanted by-products, gel extraction should be performed throughout the protocol using the QIAquick Gel Extraction Kit. Use a DNA polymerase with proof-reading activity (e.g. KOD DNA Polymerase) for all PCR reactions throughout the protocol.
4. Remove the parental plasmid by adding 1 µl DpnI per 50 µl PCR reaction product and incubating for 1-2 h at 37°C and 400 r.p.m. (Thermomixer Compact).
5. Fuse the two fragments by Gibson Assembly[38] according to the manufacturer's instructions. Note that Gibson reactions can be downscaled to 5 µl per reaction.
6. Dilute the assembled products 4-fold with H_2O, add 2 µl of the diluted product to 50 µl chemically competent Top10 cells and transform the cells according to the manufacturer's instructions.
7. Incubate the cells for 1 h at 37°C, 220 r.p.m. (incubator SI500) and spread them onto LB plates supplemented with 100 µg ml^{-1} ampicillin.
8. Grow the cells overnight at 37°C.
9. The next day, pick single colonies and grow them in 5 ml 2×TY supplemented with 100 µg ml^{-1} ampicillin overnight at 37°C and 220 r.p.m. (incubator SI500).

10. Extract the phagemid DNA (QIAprep Spin Miniprep Kit) according to the manufacturer's instructions and confirm the nucleotide sequences by DNA sequencing using the primers pLITMUS-F and pLITMUS-R (**Table 1**).

Combinatorial library cloning on phagemids • TIMING 2 weeks

11. Design and order user-specific forward and reverse primers for the amplification of the PM vector backbone (e.g. pLITMUS-Lib-F and pLITMUS-Lib-R; **Supplementary Table 2**) and the insertion of the randomized target sequence (e.g. Library 1-F, Library 1-R; **Supplementary Table 2**). PCR primers for insert amplification require a 15-25 bp overlap with each other as well as a 15-25 bp overlap with the amplified vector backbone. ▲**CRITICAL STEP** Avoid randomized library positions within the primer overlap regions.

12. Amplify the PCR fragments (see Equipment Setup) and purify the samples using the QIAquick PCR Purification Kit or the MinElute PCR Purification Kit (for samples <100 bp). ▲**CRITICAL STEP** The PCR product concentration affects the efficiency of the assembly reaction. Optimized cloning efficiency requires at least 20 ng μl^{-1} of the PM vector backbone.

13. Add 1 µl DpnI per 50 µl PCR reaction product and incubate for 1-2 h at 37°C and 400 r.p.m. (Thermomixer Compact).

14. Fuse the DNA fragments by Gibson Assembly[38]. Upscale Gibson reactions (e.g. 4 × 20 µl) to increase the total plasmid concentration.

15. Pool the Gibson reactions, purify the assembled plasmid using the QIAquick PCR Purification Kit and elute in 30 µl H_2O. ▲**CRITICAL STEP** Note that purification is important to decrease the salt concentration and to decrease the Gibson reaction components as these are toxic to the cells at high concentrations.

16. Measure the plasmid concentration with a spectrophotometer (NanoDrop Lite). ▲**CRITICAL STEP** DNA concentrations should be >10 ng μl^{-1} for high transformation efficiency.

17. Transform 1-2 µl of DNA into 50 µl electrocompetent cells (DH5-alpha or TG1) and add 950 µl S.O.C medium. ▲**CRITICAL STEP** Use electroporation as the method of choice for transformation as it allows much larger library sizes.

18. Incubate for 1 h at 37°C, 220 r.p.m. (incubator SI500).

19. Plate the transformation reaction on Nunc Square BioAssay Dishes (24.1 cm × 24.1 cm) supplemented with 100 µg ml^{-1} ampicillin and incubate overnight at 37°C.

20. The next day, harvest the cells with a cell spreader. ▲**CRITICAL STEP** Only use plates with more than 10^5 clones. The transformation efficiency should be estimated by plating

serial dilutions (10^{-2} and 10^{-4} in 2×TY) on additional petri dishes (57 cm^2) supplemented with 100 µg ml^{-1} ampicillin and colony counting the following day. Ideally, to cover the whole library space, at least a 3-fold excess of colonies relative to the theoretical library size is desired. **? TROUBLESHOOTING**

21. Purify the combinatorial DNA library using the HiSpeed Plasmid Maxi Kit and elute in 0.5 ml TE buffer. Measure the plasmid concentration with a spectrophotometer (NanoDrop Lite). The obtained plasmid concentration should ideally be >50 ng ml^{-1}.

22. Pick individual colonies (10-100 clones of a library depending on the library size and quality control desired) from the petri dishes which were used to estimate the transformation efficiency (see Step 20) and culture each in 5 ml 2×TY supplemented with 100 µg ml^{-1} ampicillin overnight at 37°C, 220 r.p.m. (incubator SI500). The next day, extract phagemid DNA (QIAprep Spin Miniprep Kit) and sequence the gene of interest using the primers pLITMUS-F and/or pLITMUS-R to confirm library diversity (**Table 1**). **? TROUBLESHOOTING**

Production of M13 phage from a combinatorial phagemid library • TIMING 1 week

23. Transform 50 µl chemically competent Top10 cells with equal moles of HP (M13KO7-ΔPS-ΔgeneIII-ΔgeneVI) and AP (pJPC12-ΔPS-P_{RM}-B0034-geneVI) (10-20 fmol per plasmid, typically 1-2 µl in total). Note that the P_{RM} promoter can be replaced by an alternative promoter (e.g. T7) to obtain higher phage titers in the absence of the activator λ cI.

24. Add 250 µl S.O.C. medium to the samples and incubate for 1 h at 37°C, 220 r.p.m. (incubator SI500).

25. Spread the cells on LB plates supplemented with 25 µg ml^{-1} chloramphenicol and 50 µg ml^{-1} kanamycin. Grow overnight at 37°C.

26. The next day, pick a single colony, grow in 2×TY supplemented with 12.5 µg ml^{-1} chloramphenicol and 25 µg ml^{-1} kanamycin at 37°C, 250 r.p.m. (incubator SI500) until the OD_{600} reaches 0.4-0.6 (mid-exponential phase) and make cells electrocompetent as described in Gonzales *et al.*[42].

■ **PAUSE POINT** Stored electrocompetent cells can be used for the construction of any phage library.

27. Transfer 50 µl of the electrocompetent cells to a prechilled 1.5 ml tube on ice and add 1-2 µl of the cloned combinatorial phagemid library.

28. Electroporate cells, add immediately 950 µl S.O.C. medium and incubate for 1 h at 37°C, 220 r.p.m. (incubator SI500).

29. Estimate the actual phage library by colony counting of serial dilutions (10^{-2} and 10^{-4} in 2×TY) on LB plates supplemented with ampicillin (see step 20). ▲**CRITICAL STEP** Make sure not to lose any library members through low transformation efficiencies. **? TROUBLESHOOTING**

30. Add 3 ml 2×TY supplemented with 12.5 µg ml^{-1} chloramphenicol, 25 µg ml^{-1} kanamycin, and 50 µg ml^{-1} ampicillin to the transformation reaction and grow for 18-20 h at 30°C, 250 r.p.m. (incubator SI500). Note that the volume can be adjusted depending on the desired volume of the phage titer.

31. The next day, centrifuge sample for 5 min at 5,000 g.

32. Sterile-filter the phage supernatant (0.22 µm pore size). ■ **PAUSE POINT** The phage library can be kept at 4°C for short-term storage (weeks) or at -20°C for the long-term (years).

Phage titer analysis • **TIMING 3 d**

33. Streak out TG1 cells from a glycerol stock (~1-5 µl) on an M9 minimal medium plate and incubate overnight at 37°C. Note that TG1 plates can be used for a minimum of two weeks when stored at 4°C. ▲**CRITICAL STEP** Use M9 minimal medium plates to select F-pilus positive TG1 cells.

34. The next day, pick 1-4 single isolated colonies from the M9 minimal medium plate and inoculate in 10 ml 2×TY medium in a 50 ml conical centrifuge tube.

35. Incubate at 37°C and 250 r.p.m. (incubator SI500) until the OD_{600} reaches 0.4-0.6 (mid-exponential phase). It typically takes 4-6 hours for the culture to reach the desired OD_{600}. ▲**CRITICAL STEP** Do not let the cells grow into stationary phase as TG1 cells tend to lose the F' episome and this lowers the overall infection rate.

36. In the meantime, prepare serial dilutions (10^{-2}, 10^{-4}, 10^{-6}, 10^{-8} in 2×TY) of the phage library in sterile 1.5 ml tubes. Phage stocks are diluted before infection to ensure that each cell is only infected by one phage particle (number of colonies on plates equal number of phage particles).

37. Add 100 µl of the phage dilutions to 900 µl TG1 cells in a sterile microcentrifuge tube. Mix gently and incubate the samples for 1 h at 37°C with no shaking. Plate 100 µl cell suspension on prewarmed LB plates supplemented with 100 µg ml^{-1} ampicillin and incubate overnight at 37°C.

38. The next day, count the number of colonies and calculate the phage titer (**Equation 1**). Ideally, use the plates containing 20 to 400 colonies. Note that the 100-fold dilution (step 37) has to be taken into consideration.

Phage titer per ml = dilution factor x 100 x number of colonies on plate (**Equation 1**)

▲ **CRITICAL STEP** The phage titer should lie between 10^8-10^{13} colony-forming units (cfu) per ml.

Construction of accessory and reporter plasmids • TIMING 2 weeks

39. Order user-specific forward and reverse primers to replace the P_{RM} promoter on the AP plasmid (pJPC12-ΔPS-P_{RM}-B0034-geneVI) with a different promoter or inducible input. For vector amplification, use primers B0034-gVI-F and gVI-R that bind upstream and downstream of P_{RM} (**Supplementary Table 2**). For insert amplification make sure to add a 15-25 bp overlap for assembly. Optional: Clone the same inducible input into pJPC12-ΔPS-mCherry-P_R/P_{RM}-GFP to obtain a reporter for the functional characterization of selected proteins. Use primers GFP-F and mCherry-R for vector amplification (**Supplementary Table 2**).

40. Clone the accessory and reporter plasmids as described in steps 3-10. Use sequencing primers pJPC12-F and/or pJPC12-R for gene VI constructs and pJPC12-F2 for reporters (**Table 1**).

Preparation of host cells for directed evolution • TIMING 3 d

41. Transform 50 µl competent TG1 cells with equal moles of HP M13KO7-ΔPS-ΔgeneIII-ΔgeneVI and the cloned accessory plasmid (AP) (10-20 fmol per plasmid, typically 1-2 µl in total). ▲ **CRITICAL STEP** Always use an *E. coli* strain that contains the F-factor needed for M13 phage infection.

42. Add 250 µl S.O.C. medium to the sample and incubate for 1 h at 37°C, 220 r.p.m. (incubator SI500).

43. Spread the cells on LB plates supplemented with 25 µg ml^{-1} chloramphenicol and 50 µg ml^{-1} kanamycin and grow cells overnight at 37°C.

44. The next day, pick a single colony and grow cells in 2 ml 2×TY supplemented with kanamycin and chloramphenicol for 4-6 h at 37°C, 250 r.p.m. (incubator SI500) until the cells reach the late-exponential phase.

45. (Optional) Make glycerol stock and store at -80°C (see Reagent Setup).

46. Make serial dilutions of the cell suspension (e.g. 10^{-6} or 10^{-8} in M9 medium) and spread the diluted cells on an M9 minimal medium plate supplemented with 25 µg ml^{-1} chloramphenicol and 50 µg ml^{-1} kanamycin. These conditions promote phage infectability by maintaining F' pili.

47. Incubate plates for 30-48 h at 37°C. Note that bacteria grow much slower on minimal media than on rich media. This plate is used as a source of fresh colonies for selection experiments and can be used for up to two weeks when stored at 4°C.

Phage-assisted batch selection • TIMING 2 weeks

48. Inoculate 10-20 ml 2×TY containing 12.5 µg ml^{-1} chloramphenicol and 12.5 µg ml^{-1} kanamycin with 1-4 colonies from prepared M9 plate (step 47) in a 50 ml tube (**Fig. 6**).

49. Grow the starter culture for 6-8 h at 37°C and 250 r.p.m. (incubator SI500) until the OD_{600} reaches 0.4-0.6.

50. Infect 10 ml of the starter culture with the combinatorial phage library at a multiplicity of infection (MOI) of 0.5-5. An excess of cell culture can be chilled on ice and then be stored at 4°C for up to one week. This culture may be used for the next rounds of selection. Note that the selection volume can be easily up- or downscaled according to the user's need.

51. Incubate the infected cells at 37°C without stirring for 5 min.

52. Incubate the sample for 18-20 h at 30°C and 250 r.p.m. (incubator SI500).

53. The next day, centrifuge the culture for 5 min at 5,000 g and transfer 1 ml of the supernatant into a sterile microfuge tube. This sample is used to start a new round of selection.

■ **PAUSE POINT** Phage supernatants for each round of selection can be stored at 4°C for short-term storage, or at -20°C for the long-term, to continue selection at a later time.

54. Infect the starter culture (step 49) at a ratio of 10^{-3}-10^{-1} (e.g. 10-1000 µl phage supernatant in 10 ml culture) for the next round of selection.

55. Run selection cycle (steps 51-54) for several rounds until the target protein(s) are enriched. This usually takes four to eight rounds depending on the target protein's activity and thus the conditional gene VI expression. ▲**CRITICAL STEP** The phage titer should ideally stay between 10^{6}-10^{12} cfu ml^{-1} after each round of the selection (see step 56). Very high infection rates (MOI >10) lead to multiple infections and thus propagation of non-functional library members ('cheaters') whereas very low rates (MOI <0.1) decrease the performance of the system. **? TROUBLESHOOTING**

56. (Optional) During the selection process, monitor the phage titer for each round by phage titer analysis (steps 33-38). **? TROUBLESHOOTING**

57. (Optional) Monitor the selection process by infecting reporter cells (TG1 with a suitable reporter plasmid, e.g. pJPC12-ΔPS-mCherry-P/$P_{M,5G6G}$-GFP) with the obtained phage titer for each round (analogous to steps 33-38). Streak out infected cells on LB plates supplemented with 25 µg ml^{-1} chloramphenicol and 100 µg ml^{-1} ampicillin and grow overnight at 37°C. The next day, analyse the plates under the UV light of a gel documentation system. Non-active library member result in red colonies while active library members lead to green colonies due to GFP activation and mCherry repression. Store plates at 4°C overnight for improved mCherry signals.

58. After selection, sterile-filter the phage supernatant (0.22 µm pore size) and serial dilute the sample with 2×TY medium before infecting TG1 cells with an OD_{600} of 0.4-0.6. Incubate the infected cells for 1 h at 37°C before plating (see step 37).

59. Select infected cells on 100 µg ml^{-1} ampicillin plates overnight at 37°C.

60. The next day, pick at least three colonies per selection and grow each colony in 5 ml 2×TY supplemented with ampicillin overnight at 37°C and 250 r.p.m. (incubator SI500).

61. The next day, extract phagemid DNA (QIAprep Spin Miniprep Kit) and sequence the gene of interest using the primers pLITMUS-F and/or pLITMUS-R (**Table 1**).

Characterization of evolved proteins (optional) • **TIMING 3 d**

62. Transform 50 µl competent TG1 cells with equal moles of a selected phagemid and a suitable reporter plasmid (e.g. pJPC12-ΔPS-mCherry-P/$P_{M,5G6G}$-GFP) (10-20 fmol per plasmid, typically 1-2 µl in total). Transform the reporter plasmid into TG1 cells and use as a control. (Optional) Delete the expression cassette rpoN-cI_{opt}-B0015 from the phagemid (e.g. pLITMUS-ΔcI_{opt}-F, pLITMUS-ΔcI_{opt}-R) and transform the obtained plasmid (pLITMUS-J23106-geneIII) together with the reporter to compensate for growth effects between control and selected phagemids.

63. Spread the cells on LB plates supplemented with 25 µg ml^{-1} chloramphenicol and 100 µg ml^{-1} ampicillin and grow the cells overnight at 37°C.

64. The next day, pick single colonies and grow in 1 ml 2×TY supplemented with 5 µg ml^{-1} chloramphenicol and 5 µg ml^{-1} carbenicillin for 4-6 h at 37°C, 250 r.p.m. (incubator SI500). Analyse at least three replicates per transformation.

65. Measure OD_{600} of each replicate (150 µl) using the Tecan Infinite M200 plate reader.

66. Dilute cultures in 2×TY supplemented with 5 µg ml^{-1} chloramphenicol and 5 µg ml^{-1} carbenicillin to a final OD_{600} of 0.01 (150 µl) in a 96-well microplate.

67. Measure the absorbance at 600 nm, green fluorescence (excitation: 485 nm, emission: 520 nm), and red fluorescence (excitation: 585 nm, emission: 625 nm) every 10 min with the Infinite M200 plate reader (37°C, shaking between readings) until the cells reach stationary phase.

68. For data analysis use fluorescence readings in the mid-exponential phase (OD_{600} of 0.2) and correct absorbance and fluorescence against readings of a TG1 culture. Normalize the fluorescence for the number of cells by dividing by the absorbance.

? TROUBLESHOOTING

Troubleshooting advice can be found in **Table 2**.

• **TIMING**

Phagemid construction by Gibson Assembly

Steps 1-2, design of primers and oligo synthesis by supplier: 1 week

Steps 3-10, cloning of phagemid: 1 week

Combinatorial library cloning on phagemids

Step 11, design of primers and oligo synthesis by supplier: 1 week

Steps 12-22, cloning of combinatorial library: 1 week

Production of M13 phage from a combinatorial phagemid library

Steps 23-32, transfer from plasmid library to phage library: 1 week

Phage titer analysis

Steps 33-38, analysis of phage concentration: 3 d

Construction of accessory and reporter plasmids (can be done in parallel with phage library cloning)

Step 39, design of primers and oligo synthesis by supplier: 1 week

Step 40, cloning of accessory plasmid and reporter plasmid: 1 week

Preparation of host cells for directed evolution (can be done in parallel after successful AP cloning)

Steps 41-47, transformation and plating of cells: 3 d

Phage-assisted batch selection

Steps 48-57, batch selections: 1 week

Steps 58-61, extraction and sequencing of selected genes: 1 week

Characterization of evolved proteins (optional)

Steps 62-68, functional characterization by reporter assay: 3 d

ANTICIPATED RESULTS

The first section of this protocol describes the construction of combinatorial libraries used for subsequent directed evolution experiments. As examples, we describe the construction of two cI_{opt} libraries which contain five randomized positions: Library 1 (45S, 46G, 47V, 48G, 55N); Library 2 (45S, 46G, 48G, 49A, 55N). Quality control sequencing of 10-100 clones of a library may be performed to confirm diversity, depending on the library size and quality control desired. For example, ten individual clones of a constructed library should ideally result in ten different variants (**Table 3**).

The second section illustrates the directed evolution of proteins based on conditional M13 phage propagation. Libraries 1 and 2 are selected against engineered promoters for six to eight rounds leading to enrichment of TFs with binding activations against their novel

promoters (**Table 4**). We frequently obtain amino acid substitutions that occur spontaneously at certain positions not covered by the combinatorial space of the library. These mutations can originate either from mutations during library cloning or from the spontaneous error rate of M13 phage replication which is ~0.0046 mutation rate per genome per replication[43]. Such mutations can provide function[1] and contribute towards directed evolution.

The last section of the protocol describes the characterization of selected TFs. The reporter assay is designed in a way that TF binding to the bidirectional promoter results in GFP activation and mCherry repression. For baseline comparison, GFP and mCherry expression is measured for each promoter in the absence of a TF. The evolved TF variants enable simultaneous activation and repression against their engineered bidirectional promoters. For the selected cI variant ($cI_{5G6G,P}$) against the bidirectional promoter $P/P_{M,5G6G}$, GFP production is upregulated 10-fold and 94% of mCherry is repressed (**Fig. 7a,b**). The evolved cI variant ($cI_{5T6T,P}$) against the bidirectional promoter $P/P_{M,5T6T}$ results in a 9-fold activation and 98% mCherry repression (**Fig. 7c,d**). This protocol further shows a method to analyse cross-reactivities for DNA-binding proteins. WT cI and cI_{opt} activate GFP 6-fold and 9-fold and simultaneously repress 90% and 82% of mCherry production on the WT P_R/P_{RM} promoter whereas this effect is not observed for any of the engineered promoter variants (**Fig. 7e,f**). The selected TFs also do not cross-react with each other, thus ensuring orthogonality.

AUTHOR CONTRIBUTIONS

AKB, AJ and MI developed the protocol. AKB performed the experiments. AKB and MI wrote the manuscript. MI and AJ supervised the project and contributed reagents, materials and analysis tools.

ACKNOWLEDGMENTS

This research was supported by the European Commission grant FP7-ICT-2013-10 (no 610730, EVOPROG). AJ was funded by FP7-KBBE (no 613745, PROMYS), H2020 Marie Sklodowska-Curie (no 642738, MetaRNA) and EPSRC-BBSRC (no BB/M017982/1, WISB center). MI is funded by New Investigator award no WT102944 from the Wellcome Trust U.K. The authors like to thank Tina Bartels and Marko Storch for their critical reading of the manuscript.

COMPETING FINANCIAL INTERESTS

The authors declare that they have no competing financial interests.

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FIGURES

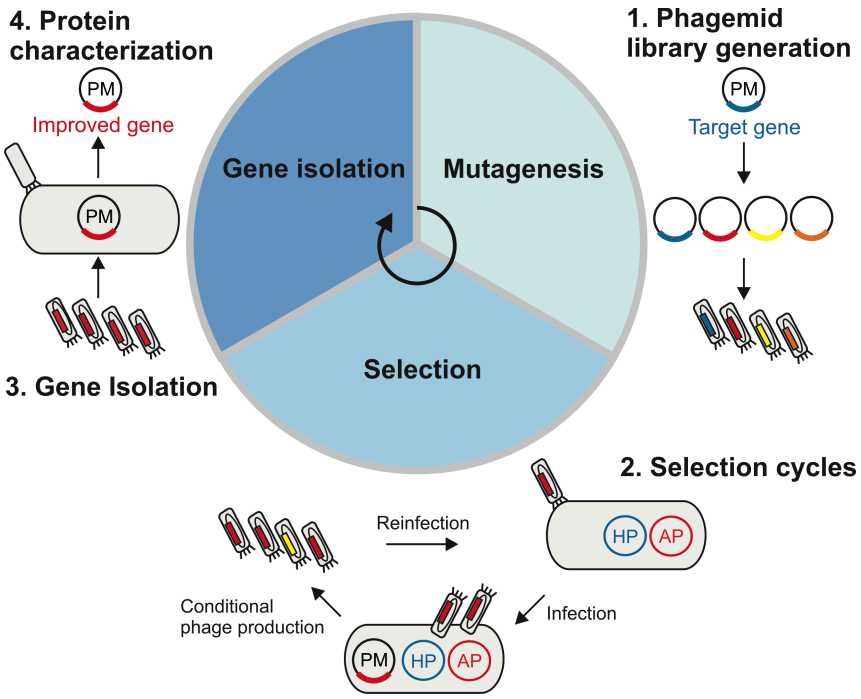


Figure 1. Intracellular directed evolution of proteins from combinatorial libraries based on conditional phage replication. 1) Phagemid library generation: A combinatorial DNA library is generated from the target gene on a phagemid (PM), which also contains conditionally expressed M13 gene III and the M13 packaging signal. The DNA library members are then packaged into phage particles which are the starting point for selection. 2) Selection cycles: TG1 cells containing a modified helper phage (HP) and an accessory plasmid (AP) are infected with the constructed phage library. The HP provides all that is required for phage propagation, except for two essential genes (gIII and gVI). The AP contains a conditional gene circuit that links the target protein's activity to conditional phage production (gene VI expression). Enrichment for a particular protein function occurs after several rounds of selection. 3) Gene isolation: Cells are infected with selected phages and the phagemid DNA is amplified and purified. 4) Protein characterization: The target protein's activity needs to be analysed using a suitable reporter assay.

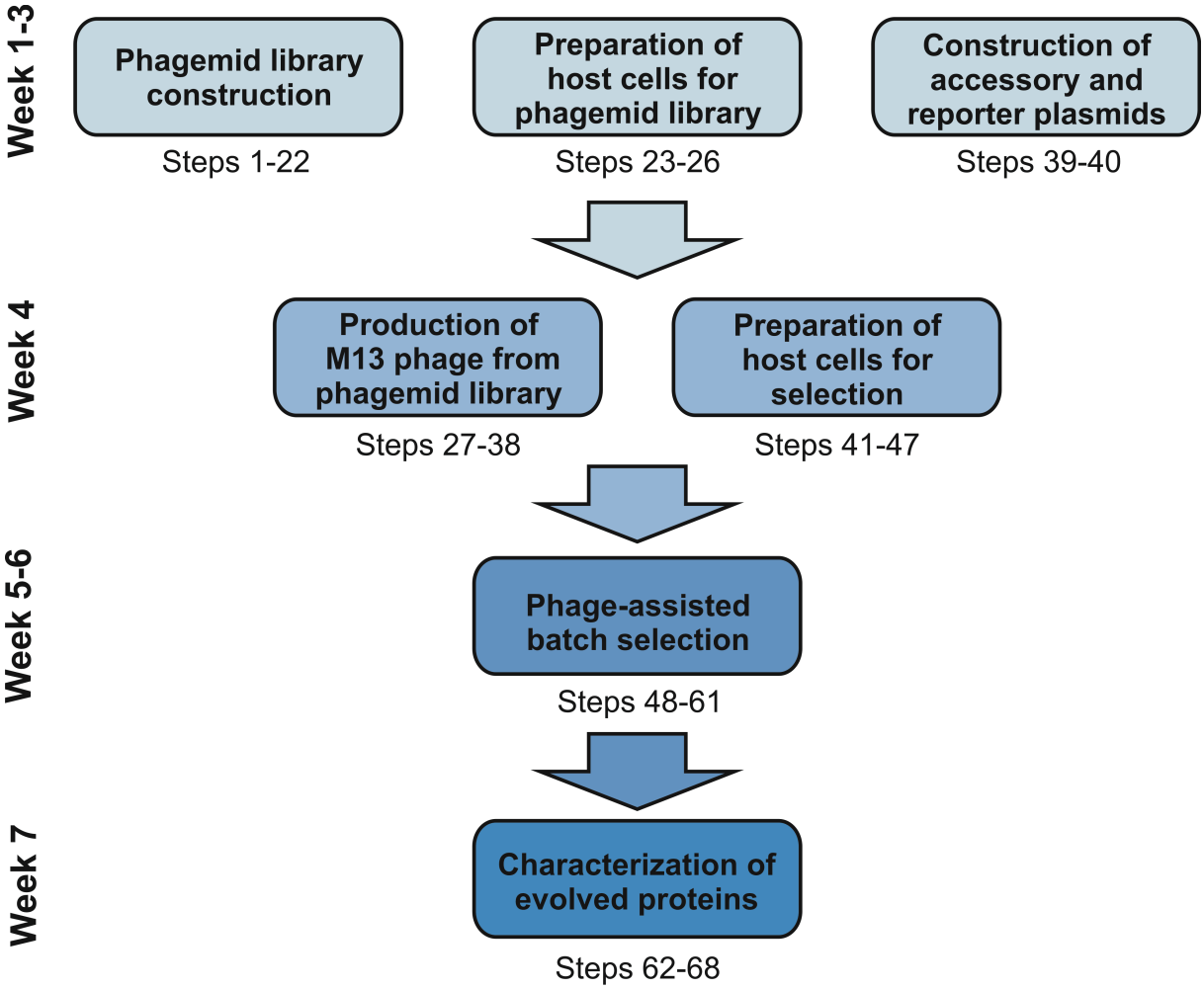


Figure 2. Flowchart and timeline of the directed evolution protocol. All major steps for design, cloning, selection and functional characterization are depicted. It takes ~7 weeks to select a candidate protein from a constructed combinatorial library.

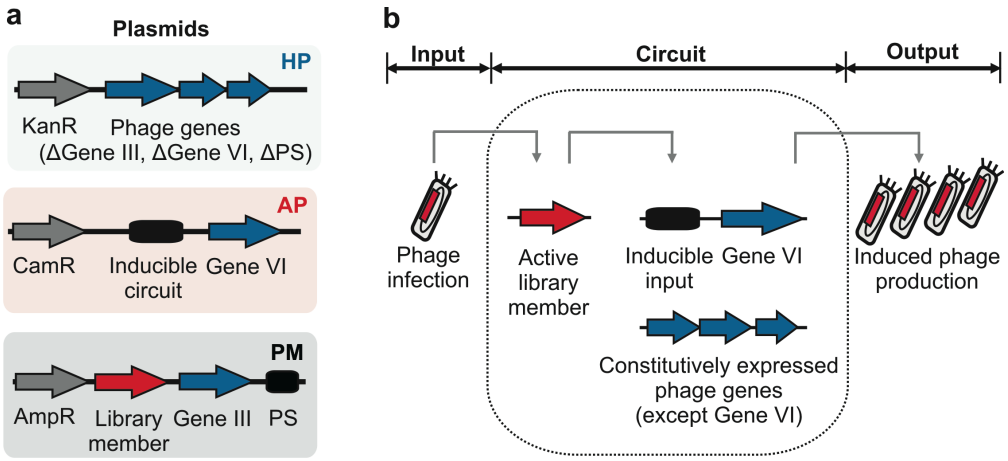


Figure 3. Directed evolution of proteins from combinatorial libraries. (**a**) Plasmids needed to set up the phagemid-based selection system. The modified helper phage HP (M13KO7-ΔPS-ΔgIII-ΔgVI) contains the kanamycin resistance gene (KanR) and all phage genes required for phage replication except the genes III and VI. The weak packaging signal (PS) is removed to prevent helper phage propagation as a phage. The accessory plasmid AP contains the chloramphenicol resistance gene (CamR) and a conditional gene VI expression circuit, induced by an active library member on the phagemid (PM). The PM also provides the ampicillin resistance gene (AmpR), the M13 packaging signal (PS; to allow DNA packaging in phage) as well as constitutively expressed gene III. (**b**) Scheme of the intracellular selection process. An active library member on the packaged PM induces gene VI expression to complete the phage life cycle, thus enriching this variant over time.

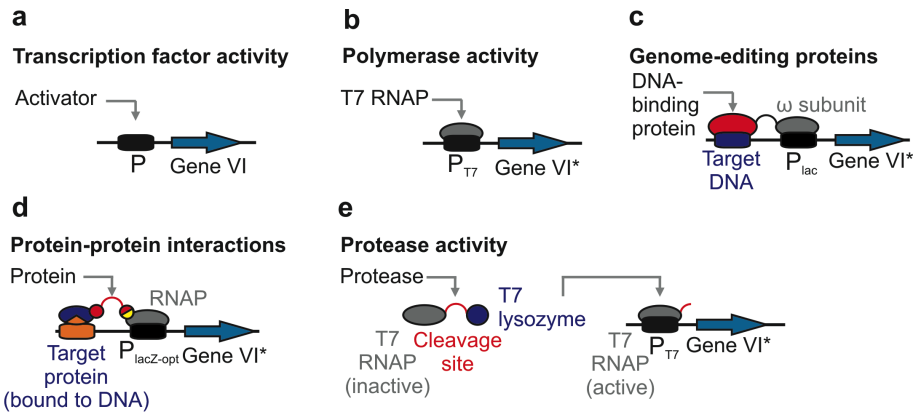
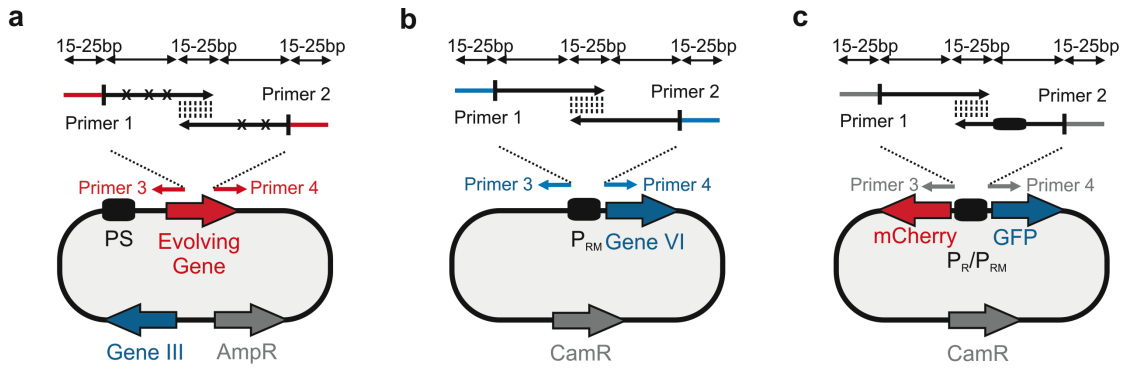


Figure 4. Linkage of an evolving protein's activity to conditional M13 phage propagation. (**a**) An evolving transcription factor[1] (e.g. λ cI) activates gene VI expression downstream of a specific promoter (e.g. λ P_{RM}). This example is depicted in this protocol by selecting new activators against engineered synthetic promoters. (**b**) An evolving RNA polymerase[22] (grey) enables transcription and hence gene VI expression. (**c**) An evolving DNA-binding protein (red) derived from genome-editing systems (transcription activator-like effector nucleases; TALENs)[11] is linked to the ω subunit of bacterial RNA polymerase III (grey). Binding to a target DNA sequence (dark blue) upstream of a minimal lac promoter (black) induces transcription of gene VI. (**d**) The target protein (dark blue) is bound to the DNA upstream the promoter $P_{lacZ\text{-}opt}$ (black) via a fused DNA-binding domain (orange) and the RNA polymerase omega subunit (RpoZ, yellow) is fused to the evolving protein (red). Target protein binding of the evolving protein[24] enables the localization of RNA polymerase upstream gene VI, initiating gene expression from the $P_{lacZ\text{-}opt}$ promoter. (**e**) The T7 polymerase (grey) is inhibited when bound to T7 lysozyme (dark blue) as it inhibits transcription initiation and the transition from initiation to elongation[44]. Proteolysis of the target cleavage site (red) by an evolving protease[23] activates the T7 RNA polymerase enabling gene VI expression downstream of the T7 promoter. Gene VI is annotated with an asterisk where originally conditional gene III was used instead of gene VI using PACE[11,22-24]. Gene III and gene VI are both minor coat proteins, each present in 3-5 copies per phage particle[21].



Phagemid (PM) **Accessory plasmid (AP)** **Reporter plasmid (RP)**

Figure 5. Experimental design and cloning strategy. (**a**) Combinatorial library construction on phagemids (PM). Randomized oligonucleotides require a 15-25 bp overlap with each other as well as a 15-25 bp overlap with the amplified vector backbone and are fused by PCR. Randomized positions are marked with an 'x' and must be avoided within overlap regions. Primers 3 and 4 bind upstream and downstream of the randomized target region and are used for vector linearization. (**b**) Accessory plasmid (AP) design. The conditional gene circuit that links an inducible input to gVI expression has to be adapted for individual needs. This is achieved by replacing the λ P_{RM} promoter with a different promoter or inducible input depending on the desired application. For example, an engineered promoter (e.g. $P_{M,5G6G}$) is constructed by overlap extension PCR and inserted into the linearized fragment by Gibson Assembly. Primers 3 and 4 bind upstream and downstream of λ P_{RM} and are used to remove the P_{RM} promoter. (**c**) Reporter plasmid (RP) design. The bidirectional λ P_R/P_{RM} is replaced by the same inducible input used on the AP (e.g. $P/P_{M,5G6G}$). The fluorescent proteins mCherry and GFP on the RP are used to characterize the activity of the selected proteins on the PM. Note that the maximum insert size using overlap extension PCR is limited by oligonucleotide synthesis (currently about 120 bp).

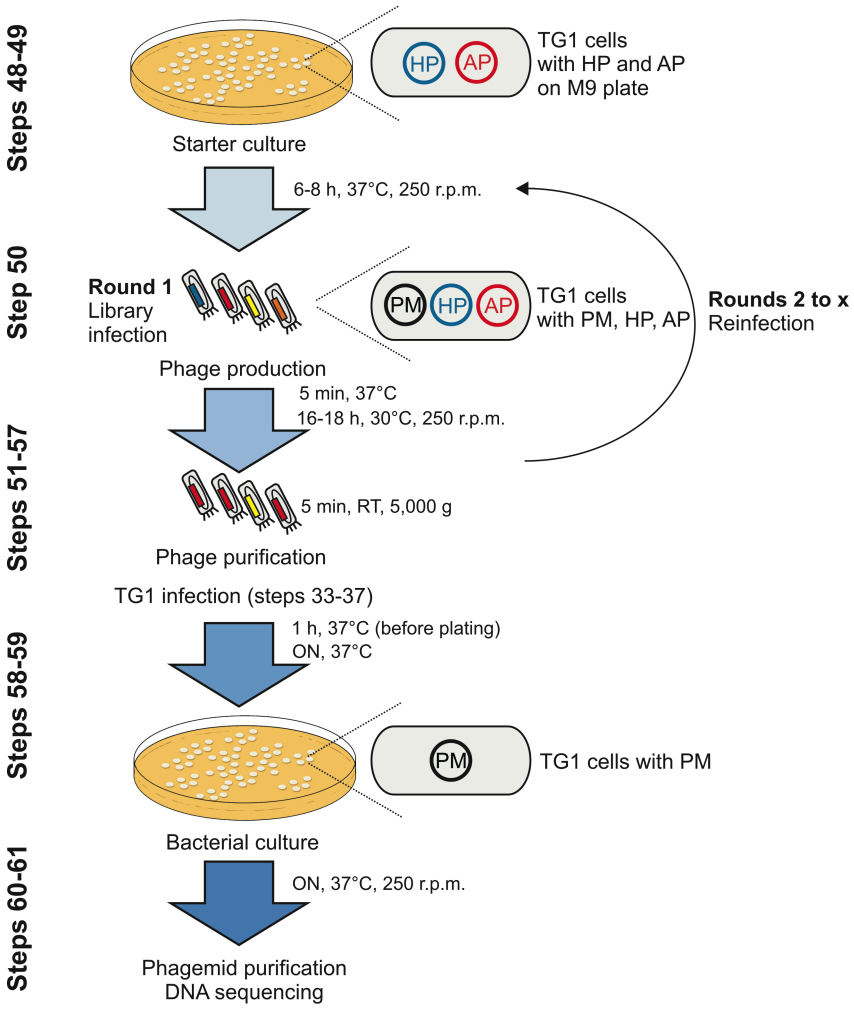


Figure 6. Phage-assisted batch selection. A starter culture from TG1 cells containing the modified M13 helper phage HP (M13KO7-ΔPS-ΔgIII-ΔgVI) and an accessory plasmid AP is prepared and cells are grown for 6-8 h at 37°C until the OD_{600} reaches 0.4-0.6. Starter cells are infected with the constructed phagemid library to start the first round of selection. Conditional phage production is performed in a shaking incubator for 16-18 h at 30°C and the resulting phage particles are separated from the cells by centrifugation. The obtained phage stock is used to start a new round of selection by infecting a fresh starter culture (= Round 2). After several rounds of reinfection and selection, a TG1 preculture is infected with the obtained phage stock and infected TG1 cells are selected on LB plates supplemented with ampicillin. Single colonies are picked and cells are grown overnight at 37°C in a shaking incubator. The next day, phagemid DNA is purified and the gene of interest is sequenced.

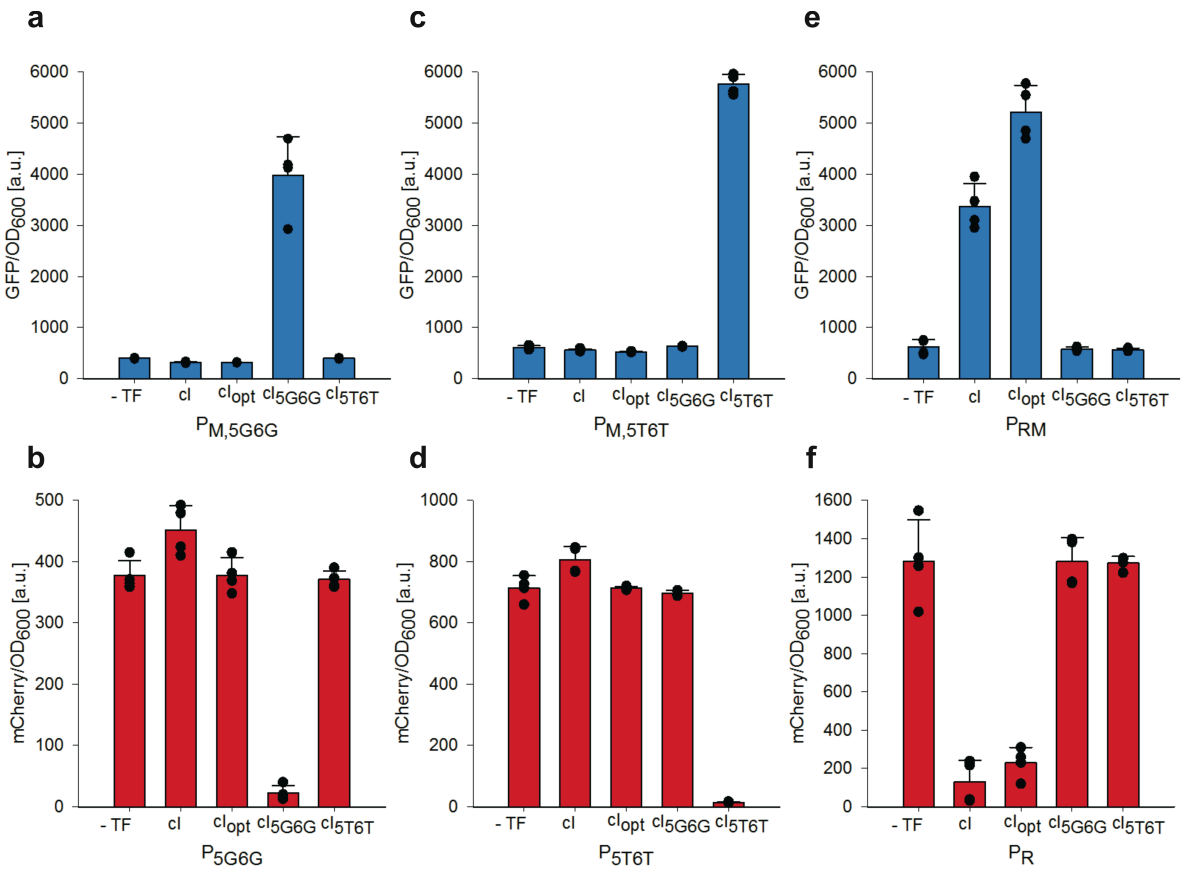


Figure 7. Dual activation and repression of engineered bidirectional λ P/P_M promoters by selected cI variants. The activity of the selected TFs needs to be verified by a reporter assay. (**a,b**) Basal promoter strength of the bidirectional promoter P/$P_{M,5G6G}$ and its dual activation and repression by the selected TF $cI_{5G6G,P}$. (**c,d**) Basal promoter strength of the bidirectional promoter P/$P_{M,5T6T}$ and its dual activation and repression by the selected TF $cI_{5T6T,P}$. (**e,f**) Basal promoter strength of P_R/P_{RM} and its activation-repression by WT λ cI and cI_{opt}. Cross-reactivity of TF variants is ruled out by reporter analysis. Basal mCherry expression varies between promoters due to base pair substitutions next to the -35 and -10 regions and y-axes are adjusted accordingly. GFP and mCherry expression was normalized to OD_{600}. Four biological replicates were measured for each sample and each replicate is represented by one dot. Error bars show 1 standard deviation.

887 # TABLES

888 **TABLE 1.** Oligonucleotides used for sequencing.

Name	Oligonucleotide sequence	Step
pLITMUS-F	5' GTC GAT TTT TGT GAT GCT CG 3'	10, 22, 61
pLITMUS-R	5' GGG TTA TTG TCT CAT GAG CGG ATA C 3'	10, 22, 61
pJPC12-F	5' AAA CGA CGG CCA GTG AGC 3'	40
pJPC12-F2	5' AGC CGT ACA TGA ACT GAG 3'	40
pJPC12-R	5' GAT AAC AAT TTC ACA CAG G 3'	40

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890 **TABLE 2.** Troubleshooting table.

Step	Problem	Possible reason	Solution
20	The transformation efficiency is too low	The DNA concentration of the cloned library too low	- Harvest and pool several transformation reactions to increase the practical library size; - Optimize the cloning procedure (e.g. PCR reactions) to increase library concentration; - Check cell competency
22	The library contains the parental plasmid	DpnI digestion was incomplete	- Gel extract the PCR-amplified pLITMUS vector backbone; - Increase DpnI incubation time to ensure complete digestion
29	The transformation efficiency is too low	The competency of prepared cells is insufficient	- Harvest and pool several transformation reactions to increase library size; - Optimize the procedure for making competent cells (e.g. do not freeze cells before transformation)
55	A large number of phages is lost during selection	The infection rate is too low	- Increase the volume of supernatant for infection; - Phage enrichment via polyethylene glycol (PEG) precipitation is generally not needed but can be performed to increase the phage titer for the next round of selection
55	The phage concentration is too high	The infection rate is too high	Decrease the volume of supernatant to lower the MOI
56	No enrichment of target proteins	The phage library does not contain functional library members	- Redesign and reconstruct the combinatorial library; - Check with a positive WT control diluted in non-functional phage (see control selections in Experimental design)

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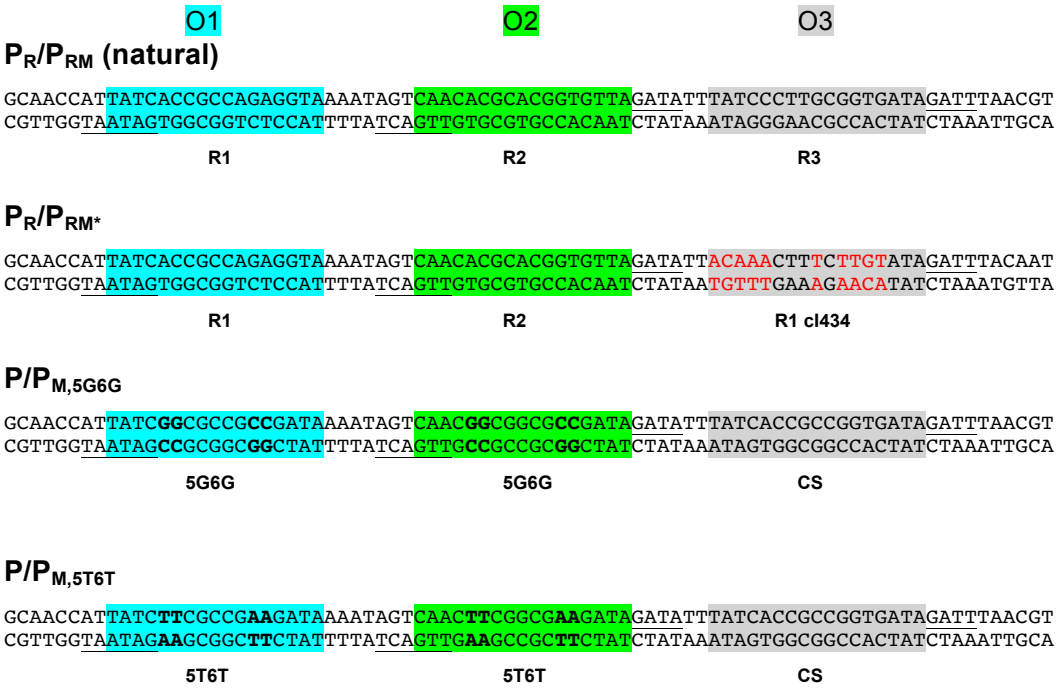
TABLE 3. Sequencing results of a combinatorial cI_{opt} library. 10 clones are shown for illustration, below. Typically 10-100 clones of a library (e.g. Library 1: 45S, 46G, 47V, 48G, 55N) may be sequenced to confirm diversity, depending on the library size and quality control desired. The obtained base pairs at the randomized NNS motifs were translated into their corresponding amino acids. Wild-type amino acids are highlighted in blue. The library contains five randomized amino acid positions known to contact promoter DNA[45-47]. This results in a combinatorial space of 3.2×10^6 variants.

Position	45	46	47	48	55
Clone 1	F	T	E	F	N
Clone 2	P	A	C	F	R
Clone 3	F	N	P	V	L
Clone 4	F	Y	L	S	M
Clone 5	G	C	L	C	A
Clone 6	I	P	M	P	T
Clone 7	F	N	P	F	N
Clone 8	S	I	G	L	Y
Clone 9	K	I	I	Y	L
Clone 10	I	T	S	I	T
Wild-type	S	G	V	G	N

TABLE 4. Sequencing results of selected TFs. Library 1 (45S, 46G, 47V, 48G, 55N) is selected against $P_{M,5T6T}$ and Library 2 (45S, 46G, 48G, 49A, 55N) against $P_{M,5G6G}$ while counterselecting against wild-type binding. Wild-type amino acids are highlighted in blue, randomized positions are underlined and the amino acid that is not part of the combinatorial library is annotated with an asterisk. Positions 35, 38, 39 illustrate the amino acid mutations in λ cI to obtain cI_{opt} and are denoted by a "P" for selected variants (e.g. $cI_{5G6G,P}$).

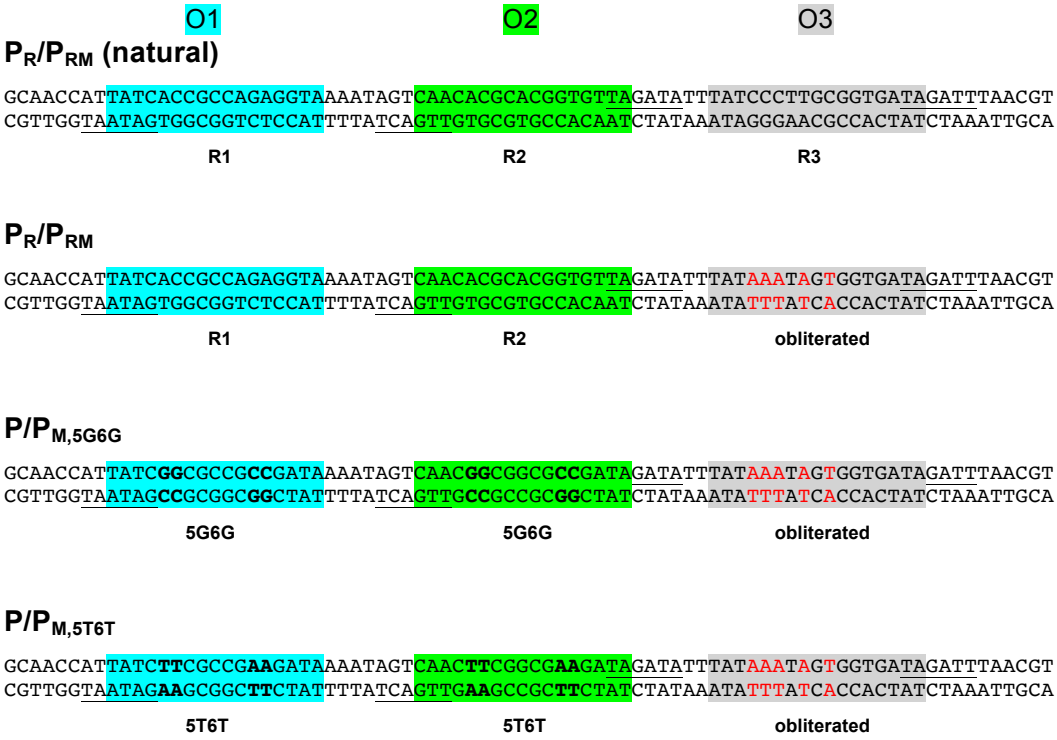
Position	35	38	39	43	44	45	46	47	48	49	55
cI	S	D	K	G	Q	S	G	V	G	A	N
cI_{opt}	L	Y	E	G	Q	S	G	V	G	A	N
$cI_{5G6G,P}$	L	Y	E	G	Q	S	A	V	S	E	W
$cI_{5T6T,P}$	L	Y	E	W*	Q	N	R	I	C	A	A

Supplementary Information



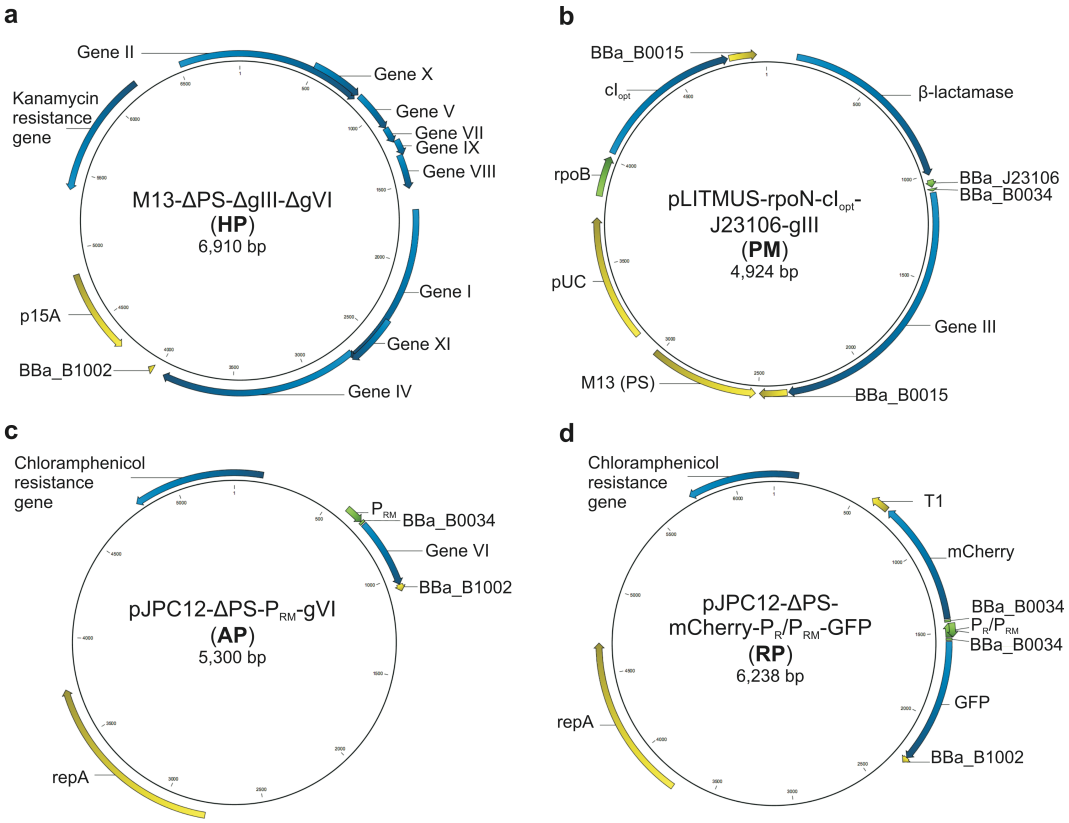
Supplementary Figure 1. Sequences of engineered promoters used for phage-assisted selections. The natural operator O3 of P_R/P_{RM} is replaced by the natural operator OR1 from cI434 in pJPC12-ΔPS-P_{RM}-B0034-geneVI (Addgene plasmid ID: 80858) in order to bypass autorepression at high cI concentration (mismatches are shown in red). Synthetic promoters are derived from the consensus sequence CS (TATCACCGCCGGTGATA) of bacteriophage λ operators. Mutated base pairs in O1 and O2 of synthetic promoters are bold and the engineered promoters are named after the position of the base substitution in the consensus half-site. WT cI binding to O3 was restored for counterselections by inserting the CS at O3. For selections, the promoter variants are used as unidirectional promoters with M13 gene VI downstream P_M variants on the accessory plasmid. Operators are highlighted as follows: O1 blue, O2 green, O3 grey.

Nature Protocols: doi:10.1038/nprot.2017.084



Supplementary Figure 2. Sequences of synthetic promoters used for functional characterization of selected TF variants. The natural operator O3 of P_R/P_{RM} is replaced by an obliterated O3 site[1] in order to bypass autorepression at high cI concentration. Synthetic promoters are derived from the consensus sequence CS (TATCACCGCCGGTGATA) of bacteriophage λ operators. Mutated base pairs in O1 and O2 of synthetic promoters are bold and the engineered promoters are named after the position of the base substitution in the consensus half-site. For functional characterization of selected TFs, the bidirectional promoter variants are used upstream of GFP and mCherry on the reporter plasmid. Operators are highlighted as follows: O1 blue, O2 green, O3 grey.

Nature Protocols: doi:10.1038/nprot.2017.084



Supplementary Figure 3. Plasmid maps needed to set up the directed evolution system. (**a**) The modified helper phage HP (M13KO7-ΔPS-ΔgeneIII-ΔgeneVI) contains all phage genes required for phage replication except the genes III and VI. The weak packaging signal (PS) is removed to bypass helper phage propagation. (**b**) The phagemid pLITMUS-rpoN-cI_{opt}-J23106-gIII provides the gene of interest cI_{opt}, the M13 packaging signal (PS) as well as constitutively expressed gene III. (**c**) The accessory plasmid pJPC12-ΔPS-P_{RM}-gVI contains a conditional gene VI expression circuit, induced by an active library member on the phagemid. (**d**) The reporter plasmid pJPC12-ΔPS-mCherry-P_R/P_{RM}-GFP is used to characterize the selected library members. For additional information on the pJPC12 vector see reference [2]. DNA sequences are shown in **Supplementary Data 1-5**.

Nature Protocols: doi:10.1038/nprot.2017.084

Supplementary Table 1. Plasmids used in this protocol. A minimal set of four plasmids (annotated with an asterisk) is required to set up the entire selection system plus subsequent reporter analysis (**Supplementary Fig. 3**). Sequences and plasmid maps, as well as DNA plasmids have been deposited and are available from Addgene (https://www.addgene.org/). For a more comprehensive list of deposited plasmids see reference [3].

Plasmid	Class	Antibiotic resistance	Addgene ID
M13KO7-ΔPS-ΔgeneIII-ΔgeneVI*	HP	Kanamycin	80840
pLITMUS-J23106-geneIII	PM	Ampicillin	
pLITMUS-rpoN-cI-J23106-geneIII	PM	Ampicillin	80843
pLITMUS-rpoN-cI_{opt}-J23106-geneIII*	PM	Ampicillin	80852
pLITMUS-rpoN-$cI_{5G6G,P}$-J23106-geneIII	PM	Ampicillin	80861
pLITMUS-rpoN-$cI_{5T6T,P}$-J23106-geneIII	PM	Ampicillin	
pJPC12-ΔPS-P_{RM}-B0034-geneVI*	AP	Chloramphenicol	80858
pJPC12-ΔPS-$P_{M,5G6G}$-O_{CS}3-B0034-geneVI	AP	Chloramphenicol	
pJPC12-ΔPS-$P_{M,5T6T}$-O_{CS}3-B0034-geneVI	AP	Chloramphenicol	
pJPC12-ΔPS-mCherry-P_R/P_{RM}-GFP*	RP	Chloramphenicol	80859
pJPC12-ΔPS-mCherry-P/$P_{M,5G6G}$-GFP	RP	Chloramphenicol	80911
pJPC12-ΔPS-mCherry-P/$P_{M,5T6T}$-GFP	RP	Chloramphenicol	

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Supplementary Table 2. Primers used for cloning. The complementary sequences used for Gibson Assembly are underlined. Oligonucleotides used for combinatorial library cloning obtain NNS codons (where S = G/C) at the randomized positions.

Name	Oligonucleotide sequence	Use	Step
pLITMUS-F	5' GGT CTC CTG GCC TGC AGT AAA G 3'	PM linearization	1
pLITMUS-R	5' GTT CAG AAT CGT ACT CTC CTG C 3'	PM linearization	1
cI-F	5' GGA GAG TAC GAT TCT GAA CAT GAG CAC AAA AAA GAA AC 3'	Amplification of target gene	2
cI-R	5' CTT TAC TGC AGG CCA GGA GAC CTA TAA ACG CAG AAA GGC CC 3'	Amplification of target gene	2
pLITMUS-Lib-F	5' GCA TTA AAT GCT TAT AAC GC 3'	PM linearization for library construction	11
pLITMUS-Lib-R	5' CAT CCC CAT CTC GTA TGC 3'	PM linearization for library construction	11
Library 1-F	5' GTC GCA TAC GAG ATG GGG ATG GGG CAG NNS NNS NNS NNS GCT TTA TTT AAT GGC ATC 3'	Randomized oligos for library construction	11
Library 1-R	5' GCG TTA TAA GCA TTT AAT GCS NNG ATG CCA TTA AAT AAA GC 3'	Randomized oligos for library construction	11
Library 2-F	5' GTC GCA TAC GAG ATG GGG ATG GGG CAG NNS NNS GTT NNS NNS TTA TTT AAT GGC ATC NNS GCA TTA AAT GCT TAT AAC GC 3'	Randomized oligos for library construction	11
Library 2-R	5' GCG TTA TAA GCA TTT AAT GC 3'	Randomized oligos for library construction	11
pLITMUS-ΔcI_{opt}-F	5' TTA GAA TTC GCT GAG AGA CCG GTC TCC TGG CCT GCA G 3'	Deletion of rpoN-cI_{opt}-B0015 cassette	62
pLITMUS-ΔcI_{opt}-R	5' CTG CAG GCC AGG AGA CCG GTC TCT CAG CGA ATT CTA A 3'	Deletion of rpoN-cI_{opt}-B0015 cassette	62
B0034-gVI-F	5' AAA GAG GAG AAA TAC TAG ATG CC 3'	AP linearization	39
gVI-R	5' GTT GCG AAT TCG ATA TCA AG 3'	AP linearization	39
$P_{M,5G6G}$-O_{CS}3-gVI-F	5' CTT GAT ATC GAA TTC GCA ACC ATT ATC GGC GCC GCC GAT AAA ATA GTC AAC GGC GGC GCC GAT AGA TAT TTA TCA CCG GCG GTG ATA G 3'	Promoter insertion on AP	39
$P_{M,5T6T}$-O_{CS}3-gVI-F	5' CTT GAT ATC GAA TTC GCA ACC ATT ATC TTC GCC GAA GAT AAA ATA GTC AAC TTC GGC GAA GAT AGA TAT TTA TCA CCG GCG GTG ATA G 3'	Promoter insertion on AP	39
O_{CS}3-gVI-R	5' CAT CTA GTA TTT CTC CTC TTT ACG TTA AAT CTA TCA CCG CCG GTG ATA AAT ATC 3'	Promoter insertion on AP	39
GFP-F	5' AAA GAG GAG AAA TAC TAG ATG 3'	RP linearization	39
mCherry-R	5' GTT GCA AAG AGG AGA AAG 3'	RP linearization	39
P/$P_{M,5G6G}$-GFP-F	5' ATT CTT TCT CCT CTT TGC AAC CAT TAT CGG CGC CGC CGA TAA AAT AGT CAA CGG CGG CGC CGA TAG ATA TTT ATA AAT AGT GGT GAT AG 3'	Promoter insertion on RP	39
P/$P_{M,5T6T}$-GFP-F	5' ATT CTT TCT CCT CTT TGC AAC CAT TAT CTT CGC CGA AGA TAA AAT AGT CAA CTT CGG CGA AGA TAG ATA TTT ATA AAT AGT GGT GAT AG 3'	Promoter insertion on RP	39
P/P_{M}-GFP-R	5' CAT CTA GTA TTT CTC CTC TTT ACG TTA AAT CTA TCA CCA CTA TTT ATA AAT ATC 3'	Promoter insertion on RP	39

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Supplementary Table 3. PCR conditions specific for individual reactions.

Protocol step	Primers	Annealing temperature [°C]	Extension time [min]	Number of cycles
3	pLITMUS-F, pLITMUS-R	54	2.5	25
3	cI-F, cI-R	46	1.0	25
12	pLITMUS-Lib-F, pLITMUS-Lib-R	50	2.5	25
12	Library 1-F, Library 1-R	45	0.5	20
39	B0034-gVI-F, gVI-R	48	3.0	25
39	$P_{M,5G6G}$-O_{CS}3-gVI-F, O_{CS}3-gVI-R	54	0.5	20
39	GFP-F, mCherry-R	45	3.0	25
39	P/$P_{M,5G6G}$-GFP-F, P/P_{M}-GFP-R	46	0.5	20

Nature Protocols: doi:10.1038/nprot.2017.084

Supplementary Data 1. Sequence of the modified helper phage (HP) M13KO7-ΔPS-ΔgeneIII-ΔgeneVI. The total plasmid size is 6,910 bp. The plasmid is available from Addgene (ID 80840).

```
FEATURES             Location/Qualifiers
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                     /label="Gene II"
     gene            496..831
                     /label="Gene X"
     gene            843..1106
                     /label="Gene V"
     gene            1108..1209
                     /label="Gene VII"
     gene            1206..1304
                     /label="Gene IX"
     gene            1301..1522
                     /label="Gene VIII"
     gene            1659..2705
                     /label="Gene I"
     gene            2379..2705
                     /label="Gene XI"
     gene            2683..3963
                     /label="Gene IV"
     terminator      4039..4071
                     /label=BBa_B1002
     origin          complement(4287..4832)
                     /label="p15A ori"
     gene            complement(5382..6197)
                     /label="Kanamycin resistance"
     gene            6507..6910
                     /label="Gene II"

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 121 CGTTCGCAGA ATTGGGAATC AACTGTTACA TGGAATGAAA CTTCCAGACA CCGTACTTTA
 181 GTTGCATATT TAAAACATGT TGAGCTACAG CACCAGATTC AGCAATTAAG CTCTAAGCCA
 241 TCCGCAAAAA TGACCTCTTA TCAAAAGGAG CAATTAAAGG TACTCTCTAA TCCTGACCTG
 301 TTGGAGTTTG CTTCCGGTCT GGTTCGCTTT GAAGCTCGAA TTAAAACGCG ATATTTGAAG
 361 TCTTTCGGGC TTCCTCTTAA TCTTTTTGAT GCAATCCGCT TTGCTTCTGA CTATAATAGT
 421 CAGGGTAAAG ACCTGATTTT TGATTTATGG TCATTCTCGT TTTCTGAACT GTTTAAAGCA
 481 TTTGAGGGGG ATTCAATGAA TATTTATGAC GATTCCGCAG TATTGGACGC TATCCAGTCT
 541 AAACATTTTA CTATTACCCC CTCTGGCAAA ACTTCTTTTG CAAAAGCCTC TCGCTATTTT
 601 GGTTTTTATC GTCGTCTGGT AAACGAGGGT TATGATAGTG TTGCTCTTAC TATGCCTCGT
 661 AATTCCTTTT GGCGTTATGT ATCTGCATTA GTTGAATGTG GTATTCCTAA ATCTCAACTG
 721 ATGAATCTTT CTACCTGTAA TAATGTTGTT CCGTTAGTTC GTTTTATTAA CGTAGATTTT
 781 TCTTCCCAAC GTCCTGACTG GTATAATGAG CCAGTTCTTA AAATCGCATA AGGTAATTCA
 841 CAATGATTAA AGTTGAAATT AAACCATCTC AAGCCCAATT TACTACTCGT TCTGGTGTTT
 901 CTCGTCAGGG CAAGCCTTAT TCACTGAATG AGCAGCTTTG TTACGTTGAT TTGGGTAATG
 961 AATATCCGGT TCTTGTCAAG ATTACTCTTG ATGAAGGTCA GCCAGCCTAT GCGCCTGGTC
1021 TGTACACCGT TCATCTGTCC TCTTTCAAAG TTGGTCAGTT CGGTTCCCTT ATGATTGACC
1081 GTCTGCGCCT CGTTCCGGCT AAGTAACATG GAGCAGGTCG CGGATTTCGA CACAATTTAT
1141 CAGGCGATGA TACAAATCTC CGTTGTACTT TGTTTCGCGC TTGGTATAAT CGCTGGGGGT
1201 CAAAGATGAG TGTTTTAGTG TATTCTTTCG CCTCTTTCGT TTTAGGTTGG TGCCTTCGTA
1261 GTGGCATTAC GTATTTTACC CGTTTAATGG AAACTTCCTC ATGAAAAAGT CTTTAGCCCT
1321 CAAAGCCTCT GTAGCCGTTG CTACCCTCGT TCCGATGCTG TCTTTCGCTG CTGAGGGTGA
1381 CGATCCCGCA AAAGCGGCCT TTAACTCCCT GCAAGCCTCA GCGACCGAAT ATATCGGTTA
1441 TGCGTGGGCG ATGGTTGTTG TCATTGTCGG CGCAACTATC GGTATCAAGC TGTTTAAGAA
1501 ATTCACCTCG AAAGCAAGCT GATAAACCGA TACAATTAAA GGCTCCTTTT GGAGCCTTTT
1561 TTTTTGGAGA TTTTCAACGT GAAAAAATTA TTATTCGCAA TTCCTTTAGT TGTTCCTTTC
1621 TATTCTCACT CCGCTGAAAC TGTTGAAGGA TCCTAATCAT GGCTGTTTAT TTTGTAACTG
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1741 CTGGGTGCAA AATAGCAACT AATCTTGATT TAAGGCTTCA AAACCTCCCG CAAGTCGGGA
1801 GGTTCGCTAA AACGCCTCGC GTTCTTAGAA TACCGGATAA GCCTTCTATA TCTGATTTGC
1861 TTGCTATTGG GCGCGGTAAT GATTCCTACG ATGAAAATAA AAACGGCTTG CTTGTTCTCG
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1981 TTGATTGGTT TCTACATGCT CGTAAATTAG GATGGGATAT TATTTTTCTT GTTCAGGACT
2041 TATCTATTGT TGATAAACAG GCGCGTTCTG CATTAGCTGA ACATGTTGTT TATTGTCGTC
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2221 CTACTGTTGA GCGTTGGCTT TATACTGGTA AGAATTTGTA TAACGCATAT GATACTAAAC
2281 AGGCTTTTTC TAGTAATTAT GATTCCGGTG TTTATTCTTA TTTAACGCCT TATTTATCAC
2341 ACGGTCGGTA TTTCAAACCA TTAAATTTAG GTCAGAAGAT GAAATTAACT AAAATATATT
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Nature Protocols: doi:10.1038/nprot.2017.084

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Nature Protocols: doi:10.1038/nprot.2017.084

Supplementary Data 2. Sequence of the phagemid (PM) pLITMUS-rpoN-cI$_{opt}$-J23106-geneIII. Sequencing primers listed in Table 1 are underlined (pLITMUS-F, pLITMUS-R). The total plasmid size is 4,924 bp. The plasmid is available from Addgene (ID 80852).

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     terminator      4751..4879
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Nature Protocols: doi:10.1038/nprot.2017.084

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Nature Protocols: doi:10.1038/nprot.2017.084

Supplementary Data 3. Sequence of the phagemid (PM) pLITMUS-rpoN-cI$_{5G6G,P}$-J23106-geneIII. Sequencing primers listed in Table 1 are underlined (pLITMUS-F, pLITMUS-R). The total plasmid size is 4,924 bp. The plasmid is available from Addgene (ID 80861).

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Nature Protocols: doi:10.1038/nprot.2017.084

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Nature Protocols: doi:10.1038/nprot.2017.084

Supplementary Data 4. Sequence of the accessory plasmid (AP) pJPC12-ΔPS-P_{RM}-B0034-geneVI. Sequencing primers listed in Table 1 are underlined (pJPC12-F, pJPC12-R). The total plasmid size is 5,300 bp. The plasmid is available from Addgene (ID 80858).

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     promoter        593..683
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     RBS             684..695
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                     /label="gene 6"
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                     /label="BBa_B1002"
     origin          2794..3744
                     /label="repA"

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     241 AAAGGATCTA GGTGAAGATC CTTTTTGATA ATCTCATGAG CGGATACATA TTTGAATGTA
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Nature Protocols: doi:10.1038/nprot.2017.084

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Nature Protocols: doi:10.1038/nprot.2017.084

Supplementary Data 5. Sequence of the reporter plasmid (RP) pJPC12-ΔPS-mCherry-P_R/P_{RM}-GFP. The sequencing primer listed in Table 1 is underlined (pJPC12-F2). The total plasmid size is 6,238 bp. The plasmid is available from Addgene (ID 80859).

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Nature Protocols: doi:10.1038/nprot.2017.084

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